GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 17, 2003, 16:35:11; Search time 10 Seconds (without alignments) 1078.385 Million cell updates/sec

US-09-840-243B-11 1341

BLOSUM62 Gapop 10.0 , Gapext 0.5

Title: Perfect score: Sequence: 1 MELTQPAEDLIQTQQTPASE.....VIENHILKLFQSNLVPADPE 260

Scoring table:

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| S<br>S     | 32         | 31         | 30         | 29         | 28        | 27                 | 26         | 25         | 24        | 23         | 22         | 21    | 20         | 19         | 18         | 17         | 16         | 15        | 14         | 13         | 12         | 11       | 10         | 9          | 89         | 7          | σ          | ű          | 4.         | w                                            | . 2        | ,<br>14            | Result<br>No. |
|------------|------------|------------|------------|------------|-----------|--------------------|------------|------------|-----------|------------|------------|-------|------------|------------|------------|------------|------------|-----------|------------|------------|------------|----------|------------|------------|------------|------------|------------|------------|------------|----------------------------------------------|------------|--------------------|---------------|
| 157        | ٠          | 158.5      | •          |            | ٠         | 161                | 162        | 163        | 163       | 163        | 163        | 163.5 | 164        | 165.5      | 165.5      | 168        | 169.5      | •         | 172.5      | 173        | 175        | 176.5    | 176.5      | 181.5      | 182.5      | 183        | 184        | æ          | 193        | 202.5                                        | 1113.5     | 13                 | Score         |
| 11.7       | 11.8       | 11.8       | 11.8       | 12.0       | 12.0      | 12.0               | 12.1       | 12.2       | 12.2      | 12.2       | 12.2       | 12.2  | 12.2       | 12.3       | 12.3       | 12.5       | 12.6       | 12.6      | 12.9       | 12.9       | 13.0       | 13.2     | 13.2       | 13.5       | 13.6       | 13.6       | 13.7       | Ü          | 14.4       | 15.1                                         | 83.0       |                    | Query         |
| 775        | 1166       | 382        | 347        | 525        | 452       | 117                | 656        | 1401       | 439       | 118        | 117        | 518   | 642        | 452        | 452        | 776        | 741        | 451       | 1059       | 333        | 328        | 231      | 226        | 768        | 231        | 1862       | 1880       | 1327       | 4377       | ø                                            | 269        | 260                | Length        |
| بر         | _          | ۳          | 1          | H          | ۳         | _                  | ۲          | Н          | Н         | سر         | ۳          | 1     | _          | μ          | _          | ۲          | 1          | 1         | _          | ۳          | μ          | ۲        | m          | ٢          | μ          | 1          | ب          | ٢          | ш          | <u>,                                    </u> | ۲          | ٢                  | BG            |
| ANR5_MOUSE | TNK2_HUMAN | GABB_MOUSE | GABC_MOUSE | ASB3_MOUSE | ILK_MOUSE | MTPN_HUMAN         | FEM1_CAEEL | LATA_LATMA | AKR_ARATH | MTPN_CHICK | MTPN_MOUSE |       | YA2A SCHPO | ILK2 HUMAN | ILK1 HUMAN | ANRS HUMAN | RN5A HUMAN | ILK_CAVPO | Y379_HUMAN | ANR2_HUMAN | ANR2_MOUSE | PSDA_RAT | PSDA_HUMAN | YB23 HUMAN | PSDA_MOUSE | ANK1_MOUSE | ANK1_HUMAN | TNK1_HUMAN | ANK3 HUMAN | ANK2_HUMAN                                   | RFXK MOUSE | RFXK HUMAN         | ID            |
| mus m      | homo       | 0 mus      | 1 mus      | 2 mus      | 2 mus m   | P58546 homo sapien | _          | _          | 3 arabic  | gall       | 4 mus mu   | homo  | 1 schiz    | homo       | 8 homo     | 2 homo     | homo       | cavia     | homo       | homo       | mus r      | 3 rattu  |            | 7 home     | x2 mus r   | 7 mus m    | 7 homo     | 5271 homo  | 5 homo     | 4 home                                       | 5 mus mi   | Ol4593 homo sapien | riptio        |

| 45          | 44         | 43          | 42          | 41          | 40          | 39          | 38          | 37          | 36          | 35          | 34          |
|-------------|------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| 148.5       | 149        | 149         | 149.5       | 150.5       | 151         | 152         | 153.5       | 154         | 155         | 156.5       | 156.5       |
| 11.1        | 11.1       | 11.1        | 11.1        | 11.2        | 11.3        | 11.3        | 11.4        | 11.5        | 11.6        | 11.7        | 11.7        |
| 765         | 323        | 227         | 433         | 168         | 768         | 587         | 592         | 777         | 735         | 383         | 347         |
| _           | μ.         | Н           | Н           | بر          | Ь           | Н           | Н           | ب           | <b>p.,a</b> |             | <b>pe</b>   |
| BAR1_MOUSE  | ANKH CHRVI | PHLB_SERLI  | AS14_MOUSE  | CDN6_HUMAN  | BAR1_RAT    | ASB2_HUMAN  | V246_FOWPV  | BAR1_HUMAN  | RNSA_MOUSE  | GABB_HUMAN  | GABC_HUMAN  |
|             |            |             |             | P42773      |             |             |             |             |             |             |             |
| mus musculu | chromatium | serratia li | mus musculu | homo sapien | rattus norv | homo sapien | fowlpox vir | homo sapien | mus musculu | homo sapien | homo sapien |

## ALIGNMENTS

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                                밁
                                                                    Matches
                                                                            Query Match
Best Local
                                                                                                                                          VARSPLIC VARSPLIC
                                                                                                                                                                                                        Repeat;
Disease
                                                                                                                                                                                                          SMART; SM00248; ANN, J.

PROSITE; PS50088; ANK_REPEAT; 3.

PROSITE; PS50297; ANK_REP REGION; 1.

PROSITE; PS50297; ANK_REP REGION; 1.

PROSITE; PS50297; ANK_REP REGION; 1.

PROSITE; PS50297; ANK_REPEAT; 3.
                                                                                                                                                                                                                                                                                                         EMBL; AF094760; AAC69883.1; --
EMBL; AF105427; AAD17972.1; --
EMBL; AF105428; AAD17973.1; --
EMBL; AF077196; AAD26991.1; --
EMBL; AC003110; AAB86654.1; --
HSSP; P42773; 1BU9.
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related genes throug
RFX-B-deficient cell
                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                     Pfam; PF00023; ank; 4. SMART; SM00248; ANK; 3.
                                                                                                                                                                                                                                                                               MIM; 209920;
                                                                                                                         VARIANT
                                                                                                                                                             REPEAT
                                                                                                                                                                      REPEAT
                                                                                                                                                                               REPEAT
                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                      InterPro; IPR002110; ANK.
               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunol.
                                _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mmunol. 164:3666-3674(2000)
FUNCTION: ACTIVATES TRANSCR
                                          MELTQPAEDLIQTQQTPASELGDPEDPGEEAADGSDTVVLSLFPCTPEPVNPEPDASVSS
PQAGSSIKHSTTLTNRQRGNEVSALPATLDSLSIHQLAAQGELDQLKEHLRKGDNLVNKP
                               MELTQPAEDLIQTQQTPASELGDPEDPGEEAADGSDTVVLSLFPCTPEPVNPEPDASVSS
                                                                    260;
                                                                                                                                                                                                                                                                                               HGNC:9987; RFXANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes through exogenous
                                                                            Similarity
                                                                                                                                                                                                        mutation;
                                                                                                       260 AA;
                                                                                                                                          123
156
189
189
222
63
                                                                    Conservative
                                                                                                                                          SCID.
118
152
185
218
218
251
63
113
                                                                                                                          195
                                                                                                        28102
                                                                           100.
                                                                            .0%;
                                                                                                        MW;
                                                                    0
                                                                   Score 1341;
Pred. No. 1.6
); Mismatches
                                                                                                                                         MISSING (IN ISOFORM RFX-B-DELTA5).
SLSIHQLAAQGELDQLKEHLRKG -> C (IN ISOFORM
                                                                                                                                 RFX-B-DELTA5)
                                                                                                      -> P (IN BLS).
FTId=VAR_009941.
6280B490F54816D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   class II transactivator
                                                                                                                                                                                                                                                                                                                                                                               moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                           DB 1;
                                                                    0
                                                                   Indels
                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
tent is in
                                                                                      260;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
MBL outstation -
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                                                                   Gaps
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RESULT RESULT PARK MONOR PROPERTY AND PROPER
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                                                                                                                                                                                                                                                                                                                                       RI SUBSTRATE And regulator of raf-1.";

J. Biol. Chem. 274:14706-14715 (1999).

C. -!- FUNCTION: ACTIVATES TRANSCRIPTION FROM CLASS II MHC PROMOTERS.

C. ACTIVATION REQUIRES THE ACTIVITY OF THE MHC CLASS II

TRANSACTIVATOR (CIITA), MAY REGULATE OTHER GENES IN THE CELL (BY

C. SIMILARITY). POTENTIATES THE ACTIVATION OF RAF-1. RFX BINDS THE X:

C. BOX OF MHC-II PROMOTERS.

C. SUBUNIT: RFX CONSISTS OF AT LEAST 3 DIFFERENT SUBUNITS; RFXAP,

C. C. FYX5 AND RFX-B/RFXANK. RFX FORMS COOPERATIVE DNA BINDING

C. COMPLEXES WITH X2BP AND CEF/NF-Y. RFX ASSOCIATES WITH CIITA TO

C. FORM AN ACTIVE TRANSCRIPTIONAL COMPLEX (BY SIMILARITY). FORMS

C. -I- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.

C. -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A

C. -I- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THYMUS, LUNG AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9Z205;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein RFXANK (Regulatory factor X subunit Regulatory factor X-associated ankyrin-containing prote repeat-containing adapter protein Tvl-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Masternak K., Barras E., Zufferey M., Conrad B., Corthals G., Aebersold R., Sanchez J.C., Hochstrasser D.F., Mach B., Reith W.; "A gene encoding a novel RFX-associated transactivator is mutated the majority of MHC class II deficiency patients."; Nat. Genet. 20:273-277(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin J.-H., Makris A., McMahon C., Bear S.E., Patriotis C., Prasad V.R., Brent R., Golemis E.A., Tsichlis P.N., "The ankyrin repeat-containing adaptor protein tvl-1 is a substrate and regulator of raf-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Spleen; MEDLINE=99021383; PubMed=9806546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99262619; PubMed=10329666;
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                                                                                                                                                      DOMAIN: INTERACTS WITH RAF-1 VIA ITS C-TERMINAL ANKYRIN REPEAT DOMAIN. THE SAME DOMAIN ALSO MEDIATES ITS HOWODIMERIZATION. DOMAIN: THE THIRD ANKYRIN REPEAT IS REQUIRED FOR ASSOCIATION WITHE TWO OTHER REX SUBJUSTIS; REXS AND REXAP (BY SIMILARITY). PTM: PHOSPHORYLATED BY RAF-1.
                                                                                                                            SIMILARITY: CONTAINS 3 ANK REPEATS
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss.Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIENHILKLFOSNLVPADPE
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tvl-1 is a novel
                                                                                                                                                                                             FOR ASSOCIATION WITH SY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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Best Local
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ANKZ HUMAN STANDALL,

Q01484; Q01485;
Q01-APR-1993 (Rel. 25, Created)
Q1-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat

15-JUN-2012 (Brain ankyrin) (Ankyrin B) (Anky
                                                       "Isolation and characterization of cDNAs encoding ankyrins reveal a family of alternatively spliced J. Cell Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PROSITE; PS50297; ANK_REP_REGION; 1.

DNA-binding; Transcription regulation; Activator; Nuclear protein; Repeat; ANK repeat; Alternative splicing; Phosphorylation.

REPEAT 88 127 ANK 1.

REPEAT 132 161 ANK 2.

REPEAT 155 194 ANK 3.

REPEAT 198 227 ANK 4.

REPEAT 198 227 ANK 4.

REPEAT 198 227 ANK 4.

REPEAT 198 227 ANK 5.

REPEAT 198 210 ANK 5.
                          REVISIONS.
                                                                                                                                                            MEDLINE=91302466; PubMed=1830053; Otto E., Kunimoto M., McLaughlin
                                                                                                                                                                                                                      TISSUE=Brain stem;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      nonerythroid)
                                                                                                     human brain genes.";
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InterPro; IPR002110; ANK.
InterPro; IPR000488; Death.
InterPro; IPR000906; ZUS.
IPR000210; ank; 24.
Pfam; PF00023; death; 1.
Pfam; PF00531; death; 1.
Pfam; PF00791; ZUS; 1.
PFANTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 21.
SMART; SM00248; ANK; 21.
SMART; SM00218; ZUS; 1.
SMART; SM00218; ZUS; 1.
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EMBL; X56958; CAA40279.2; -.
EMBL; Z26634; CAB42644.1; -.
EMBL; M37123; AAA62828.1; -.
PIR; S14533; S14533.
PIR; A39643; A39643.
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                                                                                                                                               PROSITE; PS50088; ANK_REPEAT; 20.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                            Genew;
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Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization
                                                                                                                          Phosphorylation
                                                                                                                                      Cytoskeleton; Alternative
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                                                                                                                                                                                                                                                                                                                                          HSSP; P42771;
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Chan W., Kordeli E., Bennett V.;
"440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyelinated axons.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND FUNCTION (POTENTIAL).
SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Attach integral membrane proteins to elements. Also bind to cytoskeletal proteins. ALTERNATIVE PRODUCTS: 3 ISOFORM; 1 (SHOWN HERE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS
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PTM: PHOSPHORYLATED AT MULTIPLE SITES
AND EACH PHOSPHORYLATION EVENT REGULA:
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S14569; S14569.
                                                                                                                                                                                                                                                                                                                           HGNC: 493; ANK2.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                           is-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ankyrin 3 (ANK-3) (Ankyrin G).
                                                                              ANK3_HUMAN
Q12955;
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                                                                                                                                                                     115
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                                                                                                                                                                                      175 LILERDVDINIYDWNGGTPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALG
                                                                                                                                                                                                       56 D-INTCNONGLNALHLAAKEGHVGLVQELLGRGSSVDSATKKGNTALHIASLAGOAEVVK 114
                                                                                                                                                                                                                                                         55 DASVSSPQAGSSLKHSTTLTNRQRGNEVSALPATLDSLSIHQLAAQGELDQLKEHLRKGD 114
                                                                                                                                   HNQAVAILLEN 185
                                                                                                                                                   YRK-VQQVIEN 244
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          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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29.3%;
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                                                                                                                                                                                                                                                                                                               MW;
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                                                                                                                                                                                                                                                                                    Score 202.5; DB 1
Pred. No. 9.7e-08;
                                                                                                                                                                                                                                                                                                                               DEATH.

Q -> QFICKLHLPTAPPPLNEGESLVSRILQLGPPGTK
(IN ISOFORM 2).

MISSING (IN ISOFORM 2 AND ISOFORM 3).

QQ -> PE (IN REF. 1).

I -> S (IN REF. 1).

QY -> HA (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT-RICH
REPEAT A.
                                                                                                                                                                                                                                                                                                                        ļ
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                                                               52AC496C428E29D2 CRC64;
                                                                                                                                                                                                                                                                                                                       Y (IN REF. 1).
                                                                                      4377
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                               (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGION.
                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                             Length 3924;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                         234
                                                                                                                                                                       174
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Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002110; ANK.
InterPro; IPR00048; Death.
InterPro; IPR000906; ZU5.
Pfam; PP00023; ank; 24.
Pfam; PF00531; death; 1.
Pfam; PF00791; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain stem;

MEDLINE-95138709; PubMed-7836469;

MEDLINE-95138709; PubMed-7836469;

MARKYRING. A new ankyrin gene with neural-specific isoforms localized at the axonal initial segment and node of Ranvier.";

J. Biol. Chem. 270:2352-2359(1995).

-i- FUNCTION: Membrane-cytoskeleton linker.

-i- ALTERNATIVE PRODUCTS: A number of isoforms are produced by alternative splicing.

-i- TISSUE SPECIFICITY: Expressed in brain and other tissues.

-i- SIMILARITY: CONTAINS 23 ANK REPEATS.

-i- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                    Cytoskeleton;
REPEAT 10
REPEAT 13
REPEAT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                           REPEAT
REPEAT
REPEAT
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 21.
SMART; SM00005; DEATH; 1.
SMART; SM00218; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U13616; AAA64834.1; -. HSSP; P55273; 1BI8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 600465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:494; ANK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                   REPEAT
 50;
             Similarity
                                                                                                                                                                                                                                                                                                                                                             PS50088; ANK REPEAT; 21.
PS50297; ANK REP REGION; 1.
PS50017; DEATH_DOMAIN; 1.
  Conservative
                                                                                                                                                                                                                                                                                                                                                    lternative
                                               AA;
                                                        758
791
825
1898
4174
            14.4%;
28.1%;
                                               480399 MW; F42379E55768B684 CRC64;
                                                                                                                                                                                                                                                                                                                                                   splicing; Repeat; ANK repeat.
  43;
                                                                   ANK 4.

ANK 5.

ANK 6.

ANK 7.

ANK 9.

ANK 10.

ANK 11.

ANK 12.

ANK 12.

ANK 14.

ANK 15.

ANK 15.

ANK 15.

ANK 16.

ANK 17.

ANK 17.

ANK 17.

ANK 18.

ANK 19.

ANK 20.

ANK 20.

ANK 20.

ANK 20.

ANK 20.
             Score 193; DB 1; Pred. No. 6.7e-07;
                                                          DEATH
  Mismatches
                       Length 4377;
   Indels
   10;
  Gaps
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68 KHSTTLTNRQRGNEVSALPATLDSLSIHQLAAQGELDQLKEHLRKGDNLVNKPDERGFTP 127

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O95271; O95272;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15
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                                                                                                                                                                                                                                                                                                                                                                                                                            - Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21602874; PubMed=11739745; Cook B.D., Dynek J.N., Chang W., Shost: "Role for the related poly(ADP-Ribose) at human telomeres."; Mol. Cell. Biol. 22:332-342(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chi N.-W., Lodish H.F.; "Tankyrase is a golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99454782; PubMed=10523501;
Smith S., de Lange T.;
"Cell cycle dependent localization of the telomeric PARP, tankyrase,
"Conuclear pore complexes and centrosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20556282; PubMed=10988299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith S., Giriat I., Schmitt A., de Lange T.; "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres."; Science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99040105; PubMed=9822378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WNGGTPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGY-RKVQQVIEN
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    MAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci. 112:3649-3656(1999).
Upon insulin-stimulation, phosphorylated on serine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerases
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REPEAT
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Phosphorylation; Alternative splicing.
REPEAT 215 247 ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50088; ANK_REPEAT; 15.
PROSITE; PS50199; ANK_REP_REGION; 1.
PROSITE; PS50105; SAM_DOWALIN; 1.
Transferase; Glycosyltransferase; NAD; Golgi stack; Telomere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF082556; AAC79841.1; -.
EMBL; AF082557; AAC79842.1; -.
EMBL; AF082558; AAC79843.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                             MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00023; ank; 21.
Pfam; PF00536; SAM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF082559; AAC79844.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01415; ANKYRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q00420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                         137
                                                             18
                    77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: ADP-ribosylated (-auto).
SIMILARITY: BELONGS TO THE PARP FAMI
SIMILARITY: CONTAINS 15 ANK REPEATS.
SIMILARITY: CONTAINS 1 SAM DOMAIN.
CRNGDVSRVKRLVDAANVNAKDMAGRKSSPLHFAAGFGRKDVVEHLLQMGAN-VHARDDG
                                                           ASELGDPEDPGEEAADGSDTV-VLSLFPCTPEPVNPEPDASVSSPQAGSSLKHSTTLTNR
                    QRGNEVSALPATLDSLSI ----
                                        SSSSSPSSPGSSLAESPEAAGVSSTAPLGPGAAGP----GTGVPAVSGALRE---LLEA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00248; ANK; 15.
SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:11941; TNKS.
                                                                                           Similarity
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                                                                                                                        1327 AA;
                                                                                                                                             1291
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368
401
434
521
590
                                                                                 Conservative
                                                                                                                                             1291
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145
643
1327
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                                                                                                                                                                                                                                                                                781
                                                                                          13.9%;
                                                                                                                        142010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAM.
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TO THE PARP FAMILY
                   -----HQLAAQGELDQLKEHLRKGDNLVNKPDER 123
                                                                                 36;
                                                                                                                         W.
                                                                                Score 187; DB 1;
Pred. No. 3.9e~07,
6; Mismatches 11;
                                                                                                                                                  EST -> GHS (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
H->A: LOSS OF ACTIVITY; WHE
WITH A-1291.
                                                                                                                                                                                                        PARP.
POLY-HIS.
POLY-PRO.
POLY-SER.
                                                                                                                                 E->A: LOSS OF ACTIVITY; WHEN WITH A-1184.
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                                                                                112;
                                                                                                   Length 1327;
                                                                                Indels
                                                                                                                        CRC64;
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                                                                                                                                             ASSOCIATED
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                                                                                 76;
                                                                                Gaps
248
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                                                                                                                                                             Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,

RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,

RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;

Thankyrin-1 mutations are a major cause of dominant and recessive fenditary spherocytosis.";

In Harditary spherocytosis.";

In Hereditary s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANKI HUMAN STANDARD;
P16157;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=90175370; PubMed=1689849;

Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P.,

Cheung M.C., Kan Y.W., Palek J.;

"cDNA sequence for human erythrocyte ankyrin.";

Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Hematopoietic;
TISSUE=Hematopoietic;
MEDLINE=90158830; PubMed=2137557;
Lux S.E., John K.M., Bennett V.;
"Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          control proteins:";
Nature 344:36-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                      PTM: ACYLATED BY PALMITIC ACID GROUP(S)
DISBASE: Defects in ANK1 are the cause
hereditary spherocytosis (HS).
SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                             ALTERNATIVE PRODUCTS: At least 3 isoforms; 1/2.1 (shown here), 2/2.2 and 3; are produced by alternative splicing. PTM: REGULATED BY PHOSPHORYLATION.
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSTPLHLAAGYNRVRIVQLLLQHGADVHAKDKGGLVPLHNACSYGHYEVTELLKH
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 There are no
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 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                           VARSPLIC VARSPLIC
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REPEAT
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PIR; A35049; A35049.
                                                                                                                                              VARSPLIC
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                    REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00531; death; 1. PF00791; ZU5; 1.
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HGNC:492; ANK1.
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PRINTS; PRO1415; ANKYRIN.

SMART; SM00248; ANK; 22.

SMART; SM00205; DEATH; 1.

SMART; SM00205; DEATH; 1.

SMART; SM00218; ZU5; 1.

PROSITE; PS50008; ANK REPEAT; 20.

PROSITE; PS50027; ANK REP REGION; 1.

PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoskeleton; Alternative splicing; Repeat; ANK repeat; Phosphorylation; Lipoprotein; Disease mutation; Elliptocytosis;
                                                                                                                                                                                                                                                                                                                                                                                                                89 KDA DOMAIN
BINDING DOMAIN
62 KDA DOMAIN
                                                                                                                                        55 KDA REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).
               /FTId=VAR_000597
                             /FTId=VAR 000595.
V -> I (IN HS).
/FTId=VAR 000596.
R -> H (IN BRUEGGEN).
                                                                                       TVEGPLEDPSELEVDIDYFMKHSKDHTSTPNP
GLQPDLIEGRKGAQIVKRASLKRGKQ (IN IS
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H -> D (IN ISOFORM 2).
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q02357;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                             White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux "Murine erythrocyte ankyrin cDNA: highly conserved regions regulatory domain.";
                                                                                                                                                                                                                                                                                                      TISSUE=Erythrocyte;
MEDLINE=92345717; PubMed=1386265;
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                           Ankyrin 1 (Ery
ANK1 OR ANK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANK1 MOUSE
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 FGEIETVRFLLEWGADPHILAKERESALSLASTGGYTDIVG------ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 TNRQRGNEVSALPATLDSLSIHQLAAQGELDQLKEHLRKGDNLVNKPDERGFTPLIWASA 133
                                                                                                                            FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4-2, TO ALL AND TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO TO CYTOSKELETAL PROTEINS PODRIN, TUBULIN, VIMENTIN AND DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
                                                        SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                      PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY) PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMIL
European Bioinformatics Institute.
                                                                                                                   PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPLHIASRRGNVIMVRLLLDRGAQIETKTKDELTPLHCAARNGHVRISEILLDH 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGYRKVQQVIENH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARNDDTRTAAVLLQNDPNPDVLSKTGFTPLHIAAHYENLNVAQLLLLNRGASVNFTPQNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENHLEVVKFILENGANQNVATEDGFTPLAVALQQGHENVVAHLINYGTKGKVRLPALHIA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTKKGN-----TALHIAALAGQDEVVRELVNYGAN-VNAQSQKGFTPLYMAAQ 119
                                                                                                                                                                                                                                               Genome 3:281-285(1992).
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23.1%;
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Pred. No. 1.1e-06;
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D -> N (IN DUESSELDORF).
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/FTId=VAR_000601.
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A -> S (IN REF. 2).
V -> I (IN REF. 2).
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    restrictions on its
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InterPro; IPR000906; ZUS.
Pfam; PF00023; ank; 24.
Pfam; PF000531; death; 1.
Pfam; PF00791; ZUS; 1.
Pf. ANKYRIN.
SMART; SM00248; ANK; 23.
SMART; SM00248; DEATH; 1.
SMART; SM00218; ZUS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
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       192 TPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGYRKVQQVIENH 245
                          177 ARNDDTRTAAVLLQNDENPDVLSKTGFTPLHIAAHYENLNVAQLLLNRGASVNFTPQNGI
                                                                                                        69
                                                                                                                         74 TNRQRGNEVSALPATLDSLSIHQLAAQGELDQLKEHLRKGDNLVNKPDERGFTPLIWASA 133
                                                                 ENHLEVVKFLLENGANQNVATEDGFTPLAVALQQGHENVVAHLINYGTKGKVRLPALHIA 176
                                                                                    FGEIETVRFLLEWGADPHILAKERESALSLASTGGYTDIVG---
                                                                                                      TTTKKGN-----TALHIAALAGQDEVVRELVNYGAN-VNAQSQKGFTFLYMAAQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q00420;
                                                                                                                                                        Similarity
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                                                                                                                                                Conservative
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017; DEATH DOMAIN; 1.
Repeat; ANK repeat; Phosphorylation; Lipoprotein.
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Pred. No. 1.3e-06;
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                                                                                                                                                                                                          DOMAIN).
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                                                                                                                                                                                                DEATH
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                                                -----LLLERDVDINIYDWNGG 191
                                                                                                                                                 70;
                                                                                                                                                                  Length 1862;
                                                                                                                                                  Indels 74;
                                                                                         ----- 174
                                                                                                                                                 Gaps
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casayant T.,
RA Klein P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Masahima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H.,
Wang K.H., Washi Z. C., Wilhttaker C., Wilming L.,
Warnichaw-Rori's A. Vochida K., Hasanarawa V., Kawai H., Kohreniri S.,
SMART; SMO0248; ANK; 5.

PROSITE; PS50088; ANK REPEAT; 5.

PROSITE; PS50297; ANK REP_REGION; 1.

Proteasome; ANK repeat; Repeat.

REPEAT 39 68 ANK 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.",
"State 409:685-690(2001).

-!- FUNCTION: Acts as a regulatory subunit of the 26S proteasome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                     PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1858898; Psmd10.
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                                                                                                                                                                                                                                                                                                             InterPro; IPR002110; ANK. Pfam; PF00023; ank; 5.
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MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Component of the PA700 complex. SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated
                                                                                                                                                                                                                                                                                                                                                                                                                                                       P42773; 1IHB.
                                                                                                                                                                                                                                                                 PR01415; ANKYRIN.
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  (See http://www.isb-sib.ch/announce/
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PROSITE; PS50088; ANK REPEAT; 13.
PROSITE; PS50297; ANK\_REP\_REGION; 1.
Hypothetical protein; Repeat; ANK re

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Best Local
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                                                                                                                                                                                                                       InterPro; IPR002110; ANK. Pfam; PF00023; ank; 14. SMART; SM00248; ANK; 13.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20039619; PubMed=10574462;
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15-JUN-2002
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            large proteins in vitro."; Res. 6:337-345(1999).
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231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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                                             Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Acts as a regulatory subunit of the 26S pr
is involved in the ATP-dependent degradation of ubig
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINB=9838579; PubMed=9714768;
HORI T., Kato S., Saeki M., DeMartino G.N., S
Takeuchi J., Toh-E A., Tanaka K.;
"CDNA cloning and functional analysis of p28
[Nas7p], two novel regulatory subunits of the
                                                                                                                                                                                         Higashitsuji H., Fujita J.; "Enhanced expression of a novel tumour marker in the human
                                                                                                                                                                                                               TISSUE=Placenta;
                      -!- SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                               TISSUE=Lung;
                                                                                                                              Submitted (JAN-1999)
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                        Submitted (JAN-1996)
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Gene
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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REPEAT
REPEAT
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                      regulatory subunit p28) (Gankyrin).
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IS-JUN-2002 (Rel. 41, Last sequence update)
IS-JUN-2002 (Rel. 41, Last annotation update)
26S proteasome non-ATPase regulatory subunit
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                                  SUBUNIT: Component of the
                                            proteins.
   SWISS-PROT entry
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                                                                                                                             EMBL/GenBank/DDBJ
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                               PA700 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 181.5; DB 1
Pred. No. 5.1e-07;
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Best Local
                                                                                                                                                                                                            TISSUE-Placenta;
Higashitsuji H., Fujita J.;
Higashitsuji H., Fujita J.;
"Cloning of rat gankyrin homologue containing ankyrin repeats.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
26S proteasome non-ATPase regulatory subunit 10 (26S proteasome
                                                                                                                -!- SUBUNIT: Component of the PA700 complex.
-!- SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory subunit p28) (Gankyrin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
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PROSITE; PS50297; ANK_REP_REGION; 1.
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SM00248; ANK; 5.
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39 68 ANI
72 101 ANI
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105 136 ANI
138 167 ANI
171 200 ANI
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Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB022014; BAA36954.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002110; ANK. Pfam; PF00023; ank; 5. PRINTS; PR01415; ANKYRIN. SMART; SM00248; ANK; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P42773; 1IHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50088; ANK REPEAT; 5.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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                                                                      Kemp T.J., Sadusky T.J., Saltisi F., Carey N., Moss J., Sassoon D.A., Goldspink G., Coulton G.R.; "Identification of Ankrd2, a novel skeletal muscle gene stretch-responsive ankyrin-repeat protein.";
                                                                                                                             SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=129/Sv, and C57BL/10; TISSUE-Spleen, and Skeletal muscle;
MEDLINE=20334618; PubMed=10873377;
MEDLINE=20334618; PubMed=10873377;
                                                                                                                                                                                                                  TISSUE=Diaphragm;
Ievolella C., Formentin E., Lanfranchi G.;
"Characterization of a member of a new family proteins with ankyrin
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ankyrin repeat domain protein 2 (Skeletal muscle ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANR2_MOUSE
Q9WV06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
Tsukamoto Y., Senda T.,
                            SEQUENCE FROM N.A.
                                                                                                                                                                                            Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                              ANKRD2 OR ARPP
                                                           Genomics 66:229-241(2000).
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 DPHILAKERESA----LSLASTGGYTDIVGLILERDVDINIYDWNGGTPLLYAVRGNHVK 204
               PubMed=12004005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 IAVMLLEGGANPDAKNHYDATAMHRAAAKGNLKMV-----HILLFYKASTNIQDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 LDSLSIHQLAAQGELDQLKEHLRKGDNLVNKPDERGFTPLIWASAFGEIETVRFLLEWGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VSNLMVCNLAYNGKLDELKESILADKSLATRTDQDSRTALHWACSAGHTEIVEFLLQLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVEALLARGADLTTEADSGYTPMDLAVALGYRKVQQVIENHILKLFQSNLVPADPE
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                                                                                                                                                                                                                                                                                                                                                                         (mArpp)
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105
138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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134
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Nakano T.,
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ANK 2.
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Pred. No. 2.5e-07;
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Sciurognathi; Muridae; Murinae;
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 Nakada
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   Ishiguro
                                                                                                                     Yang S.Y.,
                                                                                         coding for a
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- i- FUNCTION: May play an important role in skeletal muscle
                                                                                                                                                                                                  REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ011118; CAB46646.1; -. EMBL; AJ249346; CAB99432.1; -. EMBL; AJ245514; CAB99431.1; -- HSSP; P25963; 1IKN
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                             PROSITE; PS50088; ANK REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
ANK repeat; Repeat.
                                                                                                                                                                                                                                                                                                                            InterPro; IPR002110; ANK. Pfam; PF00023; ank; 4. SMART; SM00248; ANK; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
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-!- SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1861447; Ankrd2
   212 RDKLLSTPLHVAVRTGHVEIVEHFLSLGLDINAKDREGDSALHDAVRLNRYKIIKLLLLH
                                                                                         93 SIHQLAAQGELDQLKEHLRKGDNLVNKPDERGFTPLIWASAFGEIETVRFLLEWGADPHI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypertrophy
                                LAKERESALSLASTGGYTDIVGLLLERDVDINIYDWNGGTPLLYAVRGNHVKCVEALLAR 212
                                                               ALHRASLEGHMEILEKLLENGAT-VDFQDRLDCTAMHWACRGGHLEVVRLLQSRGADTNV
                                                                                                                             49;
                                                                                                                                         Similarity
                                                                                                                                                                                                                                              Repeat.
116
149
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215
248
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                                                                                                                                                                                                      145
178
211
244
277
                                                                                                                                         13.0%;
                                                                                                                                                                                         36707 MW;
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ANK 2.
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ANK 4.
ANK 5.
                                                                                                                                         Score 175; DB 1; Length 328; Pred. No. 5.3e-07;
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                                                                                                                             Mismatches
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RAPE PRO CONTROL OF PROCESS OF PR
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(99GZV1; Q8WUD7;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ankyrin repeat domain protein 2 (Skeletal muscle protein) (hArpp).
ANKRD2 OR ARPP.
                                              Pallavicini A., Kojic S., Be.
Ievolella C., Bortoletto G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                        PubMed=11444853;
                                                                                                                                                                                                                                  TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                 Faulkner G.,
                 Valle G.;
                                                                     Bean C., Vair
3., Pacchioni
                                                                           Vainzof M., Salamon
ioni B., Zatz M., Lar
                                                                     в.,
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                                                                           Lanfranchi G.,
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272

GADMMAKNLAGKTPTDL-VQLWQADTRHALEH 302 GADLTTEADSGYTPMDLAVALGYRKVQQVIEN 244

015084; Y379\_HUMAN

STANDARD;

PRT;

1059 AA

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PROSITE; PS50297; ANK REP_REGION; 1.
ANK repeat; Repeat; Alternative spli
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:495; ANKRD2.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
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EMBL; AJ304804; CAC19411.1; -.
EMBL; AB058599; BAB60958 1; -
EMBL; BC020817; AAH20817.1; -.
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Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moriyama M., Tsukamoto Y., Fujiwara M., Kondo G
Ishiguro N., Miyazaki A., Nakamura K., Hori N.,
Takeuchi K., Satoh H., Mori S., Ito H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1), AN MEDLINE=21347023; PubMed=11453652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys.
    276
                             213 GADLTTEADSGYTPMDLAVALGYRKVQQVIEN 244
                                                                 216
                                                                                     153 LAKERESALSLASTGGYTDIVGLLLERDVDINIYDWNGGTPLLYAVRGNHVKCVEALLAR 212
                                                                                                                    157 ALHRASLEGHMEILEKLLDNGAT-VDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 285:715-723(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of a novel human ankyrin-repeated protein homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of human skeletal muscle Ankrd2.";
Biochem. Biophys. Res. Commun. 285:378-386(2001)
                                                                                                                                                 93 SIHQLAAQGELDQLKEHLRKGDNLVNKPDERGFTFLIWASAFGEIETVRFLLEWGADPHI 152
                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in skeletal and cardiac muscles Found in slow fibers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypertrophy.
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: May play an important role in skeletal muscle
GADMMTKNLAGKTPTDL-VQLWQADTRHALEH 306
                                                         RDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P80144; 2MYO
                                                                                                                                                                                                                                                                                                                                                                                                                           ; PR01415; ANKYRIN.
SM00248; ANK; 5.
                                                                                                                                                                                         49;
                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                 186
219
252
219
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                    ΑA;
                                                                                                                                                                                                                                                  37151 MW;
                                                                                                                                                                                12.9%; Score 173; DB 1; Length 333; 32.2%; Pred. No. 7.8e-07; tive 28; Mismatches 73; Indels
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ANK 2.
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ANK 4.
ANK 5.
                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM 2).
T -> A (IN REF. 3).
                                                                                                                                                                                                                                                679736F0491467A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kondo G., Nakada C., Baba T.,
Hori N., Sato K., Shomori K.,
                                                                                                                                                                               Gaps
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RESULT 14 Y379\_HUMAN

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ALD COCKER RANK KARAKARAKA COCKER PROPERTIES PROPERTIES
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16-OCT-2001
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                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50088; ANK REPEAT; 24.
PROSITE; PS50297; ANK REP REGION;
Hypothetical protein; Repeat; ANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII.
The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00023; ank; 28. SMART; SM00248; ANK; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB002377; BAA20833.2; -. HSSP; P80144; 2MYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
-i- SIMILARITY: CONTAINS AT LEAST 27 ANK REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA0379 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002110; ANK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIAA0379
       69;
                           Similarity
                                                                                1059 AA;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40,
(Rel. 40,
(Rel. 40,
                                                                                                                                     506
540
584
617
651
651
720
720
753
790
823
857
                   12.9%;
                                                                              113465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
       43;
                                                                                              Score 172.5; DB 1
Pred. No. 4.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANK repeat.
       Mismatches
                                                                                                                                                     C1F55E6CFE494770 CRC64;
                                       DB 1;
   Indels
                                       Length 1059;
   89;
Gaps
 9
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       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILK_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILK_CAVPO STANDARD; PRT; 451 AA. p57044; p57044; p6-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Integrin-linked protein kinase (EC 2.7.1.-) (
                                                                                                                                                                                                                                                                                                                                                                                      "Guinea pig beta-integrin-linked kinase.";
"Guinea pig beta-integrin-linked kinase.";
submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.

**Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.**

**Submitted Signal Transduction kinase regulating integrin-
integrin Signal Transduction. May ACT AS A MEDIATOR OF INSIDE-OUT
INTEGRIN SIGNALING. FOCAL ADHESTON PACTEIN PART OF THE CONVERGENCE
ILK-PINCH. THIS COMPLEX IS CONSIDERED TO BE ONE OF THE CONVERGENCE
POINTS OF INTEGRIN- AND GROWTH FACTOR-SIGNALING PATHWAY. COULD BE
IMPLICATED IN MEDIATING CELL ARCHITECTURE, ADHESION TO INTEGRIN
SUBSTRATES AND ANCHORAGE-DEPENDENT GROWTH IN EPITHELIAL CELLS.
PHOSPHORYLATES BETA-1 AND BETA-3 INTEGRIN SUBUNIT ON SERINE AND
THREONINE RESIDUES, BUT ALSO AKTI AND GSK3B (BY SIMILARITY).

**SUBUNIT: INTERACTS WITH COMPLASMIC DOMAIN OF BETA 1 SUBUNIT OF
INTEGRIN. COULD ALSO INTERACTS WITH BETA 2, BETA 3 AND/OR BETA 5
SUBUNIT OF INTEGRIN. ALSO INTERACTS WITH PINCH AND PARVINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase).
EMBL; AF256520; AAF70501.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Guinea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 LIDCGAIVNOKNEKGFTPLHFÄAASTHGALCLELLVGNGADVNMKSKDGKTPLHMTALHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 RFSRSQTIIQS 334
                                                                                                                                                                                                                                       -
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                                                                                                                                                                                                                                SIMILARITY: ELCATION: Cytoplasmic (By similarity).
SUBCELULAR LOCATION: Cytoplasmic (By similarity).
DOMAIN: A PH-LIKE DOMAIN IS INVOLVED IN PHOSPHATIDYLINOSITOL
PHOSPHATE BINDING (BY SIMILARITY).
PTM: AUTOPHOSPHORYLARIED ON SER/THR FAMILY OF PROTEIN KINASES.
SIMILARITY: EBLONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SIMILARITY: CONTAINS 3 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDPDEVRALIFKKEDVNFQDNEKRTPLHAAAYLGDAEIIELLILSGARVNAKDSKWLTPL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVTCKDKKSYTPLHAAASSGMISVVKYLLDLGVDMNEPNAYGNTPLHVACYNGQDVVVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRAVASCSEEAVQVLLKHSADVNARDKNWQTPLHIAAANKAVKCAEALVPLLSNVNVSDR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ASVSSPQAGSSLKHSTTLTNRQR------GNEVSALPATLDSLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------TPLLYAVRGNH-VKCVEALLARGADLTTEADSGYTPMDLAVALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPHILAKERESALSLASTGGYTDIVGLLLERDVDIN------IYDWNGG----- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGRTALHHAAFSGHGEMVKLLLSRGAN-INAFDKKDRRAIHWAAYMGHIEVVKLLVSHGA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IHQLAAQGELDQLKEHLRKGDNLVNKPDERGFTPLIWASAFGEIETVRFLLEWGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDPED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -YRKVQQVIEN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PGEEAADGSDTVVLSLFPCTPEPVNPEPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7.1.-) (Beta-integrin-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55
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Search completed: March 17, 2003, 16:40:00
                                                                                                                                                                                          Matches
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                      DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q00420; lAWC.
InterPro; IPR002110; ANK.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
pfam; pF00023; ank; 3.
pfam; PF00063; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00248; ANK; 3.

PROSITE; PS50297; ANK REPEAT; 3.

PROSITE; PS50088; ANK REPEAT; 3.

PROSITE; PS00108; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01415; ANKYRIN ProDom; PD000001; Euk pk
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                               Phosphorylation; Repeat; ANK repeat. REPEAT 33 62 ANK 1.
                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                              100 QGELDQLKEHLRKGDNLVNKPDERGFTPLIWASAFGEIETVRFLLEWGADPHILAKERES 159
                                                                                                               160
                                     130 NKYGEMPMDKAKA----PLRELLRERAEKMGONLNRIP 163
                                                                                                                                       10
                                                                                                                                                                                                     Local
                                                                                      PLHLAASHGHRDIVQKLLQYKADINAVNEHGNVPLHYACFWGQDQVAEDLVANGALVSIC
                                                                                                              ALSLASTGGYTDIVGLLLERDVDINIYDWNGGTPLLYAVRGNHVKCVEALLARGADLTTE 219
                                                                                                                                      EGNAVAVRLWLDNTENDLNQGDDHGFSPLHWACREGRSAVVEMLIMRGARINVMNRGDDT 69
                                                              ADSGYTPMDLAVALGYRKVQQVIENHILKLFQS-NLVP 256
                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                          220
451 AA;
                                                                                                                                                                                                                                                                 180
193
199
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                          Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                     3
3
3
                                                                                                                                                                                                                                                                                                                                                                                                                                     Euk_pkinase; 1.
NK; 3.
                                                                                                                                                                                                                                                       95
128
212
445
207
220
                                                                                                                                                                                                      12.6%;
                                                                                                                                                                                                                                             51308 MW;
                                                                                                                                                                                          33;
                                                                                                                                                                                                     Score 169.5; DB 1;
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                          PH-LIKE.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                     ANK 1.
                                                                                                                                                                                                                                                                                                          ANK 3
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                             72;
                                                                                                                                                                                                                   Length
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                     451;
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                                                                                                                                                                                             Gaps
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2;

Job time : 15 secs